

# Figure 9a

GAP of: Czaal47.Seq check: 446 from: 1 to: 1214  
to: Axiglcomplete.Con check: 928 from: 1 to: 3123

Symbol comparison table:  
Gencoredisk: [Gcgcore.Data.Rundata]Nwsgapdna.Cmp  
CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	10871	Length:	3123
Ratio:	8.955	Gaps:	3
Percent Similarity:	100.000	Percent Identity:	100.000

Match display thresholds for the alignment(s):

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| = IDENTITY
: = 5
. = 1

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Czaal47.Seq x Axiglcomplete.Con May 11, 2000 12:05 ..

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1 .....GCAGGAAC TTAT 12
|||||
1101 CGCGTCACTCACGGGTAGCTCATGGTCGAGCGTAGCATGCAGGAAC TTAT 1150
|||||
13 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 62
|||||
1151 TTGCCGTGCGCTCCCAGGTCTCCGCTCGCGTGCCTTCCAGTCTGTCTCAC 1200
|||||
63 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTCTAGCTAGCTAGCTGCG 112
|||||
1201 ACTAGCTGCTGTGGGACGATCGAAGTGGGTGTGTCTAGCTAGCTAGCTGCG 1250
|||||
113 CCGTGACCACGCACATGACCGCAGTGC CGCGGGGCTGATCAAGGGAAAG 162
|||||
1251 CCGTGACCACGCACATGACCGCAGTGC CGCGGGGCTGATCAAGGGAAAG 1300
|||||
163 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 212
|||||
1301 TGATCGGATGGAGCTGGAGCTCGGGCTCGCGCCGCCGAACCCGCATCAGC 1350
|||||
213 CGCTGGCTGCCGCCGCCGAGTTCGTTCGGTCTCCTCAGCAGCTCGGCTGGC 262
|||||
1351 CGCTGGCTGCCGCCGCCGAGTTCGTTCGGTCTCCTCAGCAGCTCGGCTGGC 1400
|||||
263 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 312
|||||
1401 TCGTGCGGGAACAAGAGGGTTCTCGGCGACGCGTTCGGGGCCGCCAAGGC 1450
|||||
313 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 362
|||||
1451 GGCCACGCTTCCGCTCTTCGTCTGCGAGGATGGCGACGGAGGCGGCGGCG 1500

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Figure 9b

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363 ACCGCGACCGCGACGGCGTCGTCGACCATGAACAGCAAAGCAACAA.... 408
|||||
1501 ACCGCGACCGCGACGGCGTCGTCGACCATGAACAGCAAAGCAACAAGTGA 1550

409 .....TGTACCCAGGAAGAAGAGGCTGG 431
|||||
1601 CCCAAATCCGATCCGTGGTGTGTGTAGTGTACCCAGGAAGAAGAGGCTGG 1650

432 TGGGGTGGCCGCCGGTGAAGTGC GCGCGTAGGCGTAGCTGCGGCGGCGGG 481
|||||
1651 TGGGGTGGCCGCCGGTGAAGTGC GCGCGTAGGCGTAGCTGCGGCGGCGGG 1700

482 TACGTGAAGGTGAAGCTGGAAGGGGTGCCCATCGGGCGGAAGGTGGACGT 531
|||||
1701 TACGTGAAGGTGAAGCTGGAAGGGGTGCCCATCGGGCGGAAGGTGGACGT 1750

532 GTCCATCCACGGCTCGTACCAGGAGCTGCTCCGCACGCTCGAGAGCATGT 581
|||||
1751 GTCCATCCACGGCTCGTACCAGGAGCTGCTCCGCACGCTCGAGAGCATGT 1800

582 TCCCTTCGGGTAACCAACA..... 600
|||||
1801 TCCCTTCGGGTAACCAACAAGGTGCGTACGTTCCCGGGCCGCGGCGAGCC 1850

601 .....AG 602
||
1951 CTCCCGGCACTTAACTTGGTCGCATATACTATTCTGTAACTCTGGCAG 2000

603 ATCATGCAGAAGACGAGGTGGTGGTCTCGCAGGAGCGCCGCCGTCGCCAT 652
|||||
2001 ATCATGCAGAAGACGAGGTGGTGGTCTCGCAGGAGCGCCGCCGTCGCCAT 2050

653 CCTTATGTAGTCACCTACGAGGACGGCGAAGGGGACTGGTTGCTCGTCGG 702
|||||
2051 CCTTATGTAGTCACCTACGAGGACGGCGAAGGGGACTGGTTGCTCGTCGG 2100

703 AGATGATGTGCCGTGGGA..... 720
|||||
2101 AGATGATGTGCCGTGGGAGTACGTATCAGTCACTACTACTGTCGTCTGTA 2150

721 .....GGTCTTTGTCAAGTCAGTG 739
|||||
2201 GAACTTAAAAACGACGTTGATTTCCTTGCAAGGTCTTTGTCAAGTCAGTG 2250

740 AAGCGGCTCAAGATACTTGC GTAGCCGACGGTCGGCGCCTCAGAGACGTC 789
|||||
2251 AAGCGGCTCAAGATACTTGC GTAGCCGACGGTCGGCGCCTCAGAGACGTC 2300

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Figure 9c

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790 GTGTGGTCCGTCCTCACCAGGATCGGAGCAGTGTAGTACTCCTGGGCGTCA 839
    |||||||||||||||||||||||||||||||||||||||||||||||||||
2301 GTGTGGTCCGTCCTCACCAGGATCGGAGCAGTGTAGTACTCCTGGGCGTCA 2350

840 TCTGCGTAATAACGTTGTTTCTGTCCCTGTGTGCCCGTAGCAGTACGTACT 889
    |||||||||||||||||||||||||||||||||||||||||||||||||||
2351 TCTGCGTAATAACGTTGTTTCTGTCCCTGTGTGCCCGTAGCAGTACGTACT 2400

890 GTCCTATAGTAAGCTAGCTTTTATGGGGTGCTTCAGCTTTCAGAGCATGAC 939
    |||||||||||||||||||||||||||||||||||||||||||||||||||
2401 GTCCTATAGTAAGCTAGCTTTTATGGGGTGCTTCAGCTTTCAGAGCATGAC 2450

940 GAAAGCACTGATTAGCTGCTGTCATCACATTTGGTTCGTCTTTGTGTCTGT 989
    |||||||||||||||||||||||||||||||||||||||||||||||||||
2451 GAAAGCACTGATTAGCTGCTGTCATCACATTTGGTTCGTCTTTGTGTCTGT 2500

990 ACGGTATCGCTGGCGTCAGTGTGCGGGCAGCCTAGGTGATCTAAGCATACT 1039
    |||||||||||||||||||||||||||||||||||||||||||||||||||
2501 ACGGTATCGCTGGCGTCAGTGTGCGGGCAGCCTAGGTGATCTAAGCATACT 2550

1040 TTACTATCTCAAGTTACTTTTGGTTTCCTGAGCTTGCGATGGTAATTCATA 1089
    |||||||||||||||||||||||||||||||||||||||||||||||||||
2551 TTACTATCTCAAGTTACTTTTGGTTTCCTGAGCTTGCGATGGTAATTCATA 2600

1090 TACCGTATACGTGTGTGACTCAGGGGCGAAGCTGCCCTTAAGGCACAGGGG 1139
    |||||||||||||||||||||||||||||||||||||||||||||||||||
2601 TACCGTATACGTGTGTGACTCAGGGGCGAAGCTGCCCTTAAGGCACAGGGG 2650

1140 TCACCGGACCCGATGGAATTTATCAAATCCAGTGTAATACTATTTAAC 1189
    |||||||||||||||||||||||||||||||||||||||||||||||||||
2651 TCACCGGACCCGATGGAATTTATCAAATCCAGTGTAATACTATTTAAC 2700

1190 ACTGTTTCATCAATATATTTGATTTT..... 1214
    |||||||||||||||
2701 ACTGTTTCATCAATATATTTGATTTCAATAATTCATGGAGCTGACCTTGTG 2750

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